

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/539,535A
Source: IFWP
Date Processed by STIC: 10/12/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/539,535A

TIME: 09:28:07

Input Set : A:\41384.txt

Output Set: N:\CRF4\10122006\J539535A.raw

3 <110> APPLICANT: Kloting, et al.

5 <120> TITLE OF INVENTION: Use of the Multifunctional Transcription Factor
Yin Yang 1 and

6 Variants Thereof for Treating Illnesses, Especially Type I

7 Diabetes

9 <130> FILE REFERENCE: 30572/41384

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,535A

C--> 11 <141> CURRENT FILING DATE: 2005-06-17

11 <150> PRIOR APPLICATION NUMBER: PCT/EP03/014762

12 <151> PRIOR FILING DATE: 2003-12-19

14 <150> PRIOR APPLICATION NUMBER: DE 102 61 650.7

15 <151> PRIOR FILING DATE: 2002-12-20

17 <160> NUMBER OF SEQ ID NOS: 232

19 <170> SOFTWARE: PatentIn version 3.3

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 2256

23 <212> TYPE: DNA

24 <213> ORGANISM: Rattus norv.

26 <220> FEATURE:

27 <221> NAME/KEY: Promoter

28 <222> LOCATION: (1)..(72)

30 <220> FEATURE:

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (73)..(1125)

33 <223> OTHER INFORMATION: YY1 (BB/OK)

35 <220> FEATURE:

36 <221> NAME/KEY: misc_feature

37 <222> LOCATION: (955)..(1125)

38 <223> OTHER INFORMATION: Zinc finger

40 <220> FEATURE:

41 <221> NAME/KEY: Intron

42 <222> LOCATION: (1126)..(1758)

44 <220> FEATURE:

45 <221> NAME/KEY: misc_feature

46 <222> LOCATION: (1759)..(1917)

47 <223> OTHER INFORMATION: Zinc finger

49 <220> FEATURE:

50 <221> NAME/KEY: CDS

51 <222> LOCATION: (1759)..(1938)

52 <223> OTHER INFORMATION: YY1 (BB/OK)

54 <400> SEQUENCE: 1

55 ccgcctcctc gcccgccctc ccgcagccca ggagccgagg ctgccgcggc cgtggcgggc 60

57 gagccctcag cc atg gcc tcg ggc gac acc ctc tac att gcc acg gac ggc 111

58 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly

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125 ccc aag caa ctg gca gaa ttt gcc aga atg aag cca aga aaa att aaa      927
126 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
127 270                               275                               280                               285
129 gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca      975
130 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
131                               290                               295                               300
133 aag atg ttc agg gat aac tct gct atg aga aag cat ctg cac acc cac      1023
134 Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
135                               305                               310                               315
137 ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gcg ttc gtt gag      1071
138 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
139                               320                               325                               330
141 agc tca aag cta aaa cga cac cag ctg gtt cat act gga gaa aag ccc      1119
142 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
143                               335                               340                               345
145 ttt cag gtagagccag ttctgttcc ccaaactgca agctaggggtg ctggtcaggg      1175
146 Phe Gln
147 350
149 tggttgatat caagcactat ggggcaccgg ttgggggtatt ttattcccat ccctcctgtc      1235
151 tgcttgggtt cctggttact gctcgggact gcagggtgta cagatggggg tggagggatt      1295
153 atgcaagca cccccacact aaatttctag cagggtttaca aaaactcaac agttttgttt      1355
155 tgtagtgagt agtgtgttga attactgata gagtgcctat aagtgcgtgt ggctacagct      1415
157 ccaggtgaca cttggtgctg cttatagaag actcgtgagt tgacagttgg catcactaaa      1475
159 tatcttaatc atctgtagtc tacttcttag agtgtctctg aaaacactca agctgtaaat      1535
161 ttgcactcag cacagccctt ctgtttctca agaactagcc atgggttgtt agtatcagag      1595
163 atcccagtgt gtcagttcta aaataccctc agaagggttc cagacgagga aggaggcatg      1655
165 ctccagcagaa tagtaggtgg tttccatcta agcagtgagc catcgatccc caggttctgg      1715
167 tctcatttgc caagagggtt gatattctggt ttttccttga cag tgc aca ttc gaa      1770
168                               Cys Thr Phe Glu
169                               355
171 ggc tgc ggg aag cgc ttt tca ctg gac ttc aat ttg cgc acg cat gtg      1818
172 Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg Thr His Val
173                               360                               365                               370
175 cga atc cat acc gga gac agg ccc tat gtg tgc ccc ttc gac ggt tgt      1866
176 Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe Asp Gly Cys
177                               375                               380                               385
179 aat aag aag ttt gct cag tca act aac ctg aaa tct cac atc tta aca      1914
180 Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His Ile Leu Thr
181                               390                               395                               400
183 cac gct aaa gcc aaa aac aac cag tgaaaagaag agagaagacc ttctcgaccc      1968
184 His Ala Lys Ala Lys Asn Asn Gln
185                               405                               410
187 cggaagcct cttcaggagt gtgattggga ataaatatgc ctctcctttg tatattatatt      2028
189 ctagggaagaa ttttaaaaat gaatcctaca cacttaaggg acatgttttg ataaagtagt      2088
191 aaaaatttaa aaaaataactt taataagatg acattgctaa gatgctctat ctgctctgt      2148
193 aatctcgttt caaaaacaag gtgtttttgt aaagtgtggc cccaacagga ggacaattca      2208
195 tgaacttcgc atcaaaagac aattctttat acaacagtgc taaaaatg      2256
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 411

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200 <212> TYPE: PRT
201 <213> ORGANISM: Rattus norv.
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (955)..(1125)
207 <223> OTHER INFORMATION: Zinc finger
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: (1759)..(1917)
212 <223> OTHER INFORMATION: Zinc finger
214 <400> SEQUENCE: 2
216 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met
217 1 5 10 15
220 Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
221 20 25 30
224 Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Asp Asp Asp
225 35 40 45
228 Glu Asp Asp Glu Asp Gly Gly Gly Asp His Gly Gly Gly Gly Gly
229 50 55 60
232 His Gly His Ala Gly His His His His His His His His His Pro
233 65 70 75 80
236 Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln Val
237 85 90 95
240 His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val Val
241 100 105 110
244 Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu Asp
245 115 120 125
248 Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp Tyr
249 130 135 140
252 Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly Gly
253 145 150 155 160
256 Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly Gly Lys Lys
257 165 170 175
260 Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala Ala Gly Gly
261 180 185 190
264 Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys Gln Val Gln
265 195 200 205
268 Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp Ser Ser Asp
269 210 215 220
272 Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu Gln Ile Ile
273 225 230 235 240
276 Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr Gly Lys Lys
277 245 250 255
280 Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp Pro Lys Gln
281 260 265 270
284 Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys Glu Asp Asp
285 275 280 285
288 Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr Lys Met Phe
289 290 295 300

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292 Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His Gly Pro Arg
293 305                      310                      315                      320
296 Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys
297                      325                      330                      335
300 Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys
301                      340                      345                      350
304 Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg
305                      355                      360                      365
308 Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe
309                      370                      375                      380
312 Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His
313 385                      390                      395                      400
316 Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
317                      405                      410
320 <210> SEQ ID NO: 3
321 <211> LENGTH: 2256
322 <212> TYPE: DNA
323 <213> ORGANISM: Rattus norv.
325 <220> FEATURE:
326 <221> NAME/KEY: Promoter
327 <222> LOCATION: (1)..(72)
329 <220> FEATURE:
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331 <222> LOCATION: (73)..(1125)
332 <223> OTHER INFORMATION: YY1 (SHR)
334 <220> FEATURE:
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336 <222> LOCATION: (955)..(1125)
337 <223> OTHER INFORMATION: Zinc finger
339 <220> FEATURE:
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345 <222> LOCATION: (1759)..(1917)
346 <223> OTHER INFORMATION: Zinc finger
348 <220> FEATURE:
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350 <222> LOCATION: (1759)..(1938)
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355 gagccctcag cc atg gcc tcg ggc gac acc ctc tac att gcc acg gac ggc      111
357 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly
358 1                      5                      10
360 tcg gag atg cca gcc gag atc gtg gaa ctg cat gag att gag gtg gag      159
361 Ser Glu Met Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu
362 15                      20                      25
364 acc atc ccg gtg gag act atc gag acc acg gtg gtg ggc gag gag gag      207

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,535A

DATE: 10/12/2006

TIME: 09:28:08

Input Set : A:\41384.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date